

CC HLE in the sample. This assay can also be used for the evaluation of HLE
 CC inhibitors. The antibodies may be used to diagnose and monitor diseases
 CC such as arthritis, gout, pulmonary emphysema, chronic bronchitis, cystic
 CC fibrosis, chronic obstructive pulmonary disease, bronchiectasis, adult or
 CC infantile respiratory distress syndrome and myelogenous leukaemia. See
 CC also AAB56146-81
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADSEGDPLAEGGVR 16
 DB 1 ADSEGDPLAEGGVR 16

RESULT 2
 ID AAM04619 standard; peptide; 16 AA.
 AC AAM04619;
 XX
 DT 13-AUG-1997 (first entry)

XX Fibrinopeptide A peptide for mass spectrometry analysis.
 XX
 XX Mass spectrometry; polymer analysis; biopolymer analysis.
 OS Synthetic.
 XX
 PN WO9636986-A1.
 XX
 PD 21-NOV-1996.
 XX
 PF 17-MAY-1996; 96WO-US007146.
 XX
 PR 19-MAY-1995; 95US-00446055.
 XX
 PR 19-MAY-1995; 95US-00447175.
 XX
 PA (PERS-) PERSEPTIVE BIOSYSTEMS INC.
 XX
 PI Patterson DH, Tarr GE;
 XX
 DR WPI; 1997-012308/01.

XX Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins, etc.
 PT - by obtaining mass to charge ratios of polymer fragments, pref. using
 PT mass spectrometer, and performing statistical analysis.
 XX
 XX Example 2; Page 32; 86pp; English.

XX A method of obtaining sequence information about a polymer (e.g. DNA,
 CC RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
 CC comprising monomers of known mass has been claimed. The present sequence
 CC represents a fibrinopeptide A peptide, and was used as an example as a
 CC digestion before analysis by mass spectrometry, using this novel on-plate
 CC strategy. Total sequence information from a nine well digestion can be
 CC represented in a single digestion or it is often well digestion from two or more
 CC wells. The methods, apparatus and kit (claimed) can be used for the
 CC analysis of polymers, particularly biopolymers, e.g. DNA, RNA, peptide
 CC nucleic acids, proteins, peptides and carbohydrates. It provides a rapid,
 CC automated and cost effective sequencing of polymers, with a statistical
 CC certainty
 XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSEGDPLAEGGVR 16

DB 1 ADSEGDPLAEGGVR 16

RESULT 3
 ID AAY57487 standard; peptide; 16 AA.
 AC AAY57487;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide CS-FBP-alpha SEQ ID NO:25.
 XX
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.
 XX
 PR 18-FEB-1998; 98US-00025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.
 XX
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.

XX Disclosure; Page 120; 166pp; English.
 XX
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBXBXBX and its derivatives
 CC selected from XZBXBXBXBX, BXZXB, BXZXZXB, XBBXXZBXBX and BXZBXZ;
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXBX, XBBXXBXBX, BXBXBXBX, XBBZXXBX, and
 CC XBBZXXBXBXZBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSEGDPLAEGGVR 16
 DB 1 ADSEGDPLAEGGVR 16

RESULT 4
 ID AAB56219 standard; peptide; 16 AA.
 AC AAB56219;
 XX
 AC AAB56219;

XX

DT 15-FEB-2002 (first entry)
XX Vascular dementia-associated protein isoform (VPI) 419.
DE Vascular Dementia; VD, VD-associated protein isoform; VPI; screening;
XX diagnosis; prognosis; gene therapy.
KW
XX Homo sapiens.
OS
XX MO200169261-A2.
PN
XX 20-SEP-2001.
PD
XX 14-MAR-2001; 2001MO-GB001106.
PF
XX 15-MAR-2000; 2000GB-00006285.
PR 24-NOV-2000; 2000GB-00028734.
PR 28-NOV-2000; 2000US-00724391.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX Herath HMAc, Parekh RB, Rohlf C;
PI WPI; 2001-557937/62.
DR
XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
XX Claim 6; Page 39; 151pp; English.
XX
XX The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analyzing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 83; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADGEGDPLAEGGVR 16
DB 1 ADGEGDPLAEGGVR 16
RESULT 5
AAB91959
ID AAB91959 standard; peptide; 16 AA.
XX
XX AAB91959;
AC
XX 22-JUN-2001 (first entry)
DT
XX
XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1135.
DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy1; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS

OS Synthetic.
XX
XX MO200069900-A2.
PN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000MO-US013576.
PF
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI WPI; 2001-112059/12.
DR
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
PT
XX
XX Disclosure; Page 567; 733pp; English.
PS
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxy/thiol groups on blood components to form a
CC peptide stabilized therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC ABB90829 to ABB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 83; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADGEGDPLAEGGVR 16
DB 1 ADGEGDPLAEGGVR 16
RESULT 6
ABB52337
ID ABB52337 standard; peptide; 16 AA.
XX
XX ABB52337;
AC
XX 08-FEB-2002 (first entry)
DT
XX
XX Human API-118 tryptic digest peptide #2.
DE
XX Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
XX Homo sapiens.
OS
XX MO200175454-A2.
PN
XX 11-OCT-2001.
PD
XX

PF 03-APR-2001; 2001WO-US010908.
XX
XX 03-APR-2000; 2000US-0194504P.
PR 28-NOV-2000; 2000US-0253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX (PF12) PRIZER INC.
XX
XX Durham KL, Friedman DL, Herath HMA, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
XX WPI; 2001-639384/73.
DR
XX
XX Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.
XX
XX Example; Page 33; 162pp; English.
XX
XX The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the AFs and APIs is then normalised to an
CC Expression Reference Protein Isoform (BRPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the AFs and APIs correlates with the
CC severity of Alzheimer's disease. The present sequence is a peptide
CC produced from an API by proteolysis
XX
SQ Sequence 16 AA;
XX
XX
XX Query Match 100.0%; Score 83; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADGSEGDPLAEGGVR 16
DB 1 ADGSEGDPLAEGGVR 16
XX
XX
XX RESULT 7
ABG73668
ID ABG73668 standard; peptide; 16 AA.
XX
XX ABG73668;
AC
XX
XX 11-MAR-2003 (first entry)
DT
XX
XX Linear HIV-1 gp120 V3-loop derived peptide ligand SEQ ID 11.
XX
XX
XX gp120; interaction; co-receptor; CXCR4; CCR5; refractive index; V3 loop;
KM 7-helix transmembrane receptor; glycopeptide; virucide; anti-HIV;
KM HIV infection.
XX
XX Human immunodeficiency virus 1.
OS Synthetic.
OS
XX
XX DE10113042-A1.
PN
XX
XX 26-SEP-2002.
PD
XX
XX 09-MAR-2001; 2001DE-01013042.
PF
XX
XX 09-MAR-2001; 2001DE-01013042.
PR
XX
XX (NOCH-) NOCHT INST TROPENMEDIZIN BERNHARD.
XX
XX Schreiber M, Seifert A, Meyer B;
PI
XX
XX WPI; 2002-752120/82.
DR
XX

PT Identifying compounds that modify interaction of gp120 and co-receptors,
PT useful potentially for treating human immune deficiency virus infection,
PT also new peptides.
XX
XX Claim 10; Page 56; 68pp; German.
XX
XX
XX This invention describes novel substances that modify the interaction
CC between the gp120 protein of human immunodeficiency virus (HIV), or its
CC fragments, with the co-receptors CXCR4, CCR5 and/or other 7-helix
CC transmembrane receptors for HIV. The method comprises (a) immobilizing a
CC ligand for the co-receptor on a solid surface; (b) contacting the ligand
CC with suspended cells that express the co-receptor; and (c) determining
CC interaction by measuring the refractive index (RI) by plasmon resonance.
CC The procedure is repeated using cells that have been incubated with a
CC test compound, and this is identified if RI is lower for cells
CC preincubated with it. The ligand is a linear or cyclic (glyco)peptide
CC that includes the amino acid sequence of an HIV V3 loop (including
CC flanking Cys). The products of the invention have virucide and anti-HIV
CC (human immunodeficiency virus) activity and are useful for prevention
CC and/or treatment of HIV infection. This sequence represents a linear HIV-
CC 1 gp120 V3-loop derived peptide ligand described in the disclosure of the
CC invention
XX
SQ Sequence 16 AA;
XX
XX
XX Query Match 100.0%; Score 83; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADGSEGDPLAEGGVR 16
DB 1 ADGSEGDPLAEGGVR 16
XX
XX
XX RESULT 8
ABG78799
ID ABG78799 standard; peptide; 16 AA.
XX
XX ABG78799;
AC
XX
XX 29-NOV-2002 (first entry)
DT
XX
XX Multiple sclerosis associated feature (MSF) tryptic digest peptide #287.
XX
XX
XX Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;
KM human; multiple sclerosis-associated protein isoform; MSPI;
KM antiinflammatory; neuroprotective.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200259604-A2.
PN
XX
XX 01-AUG-2002.
PD
XX
XX 25-JAN-2002; 2002WO-GB000330.
PF
XX
XX 26-JAN-2001; 2001US-0264404P.
PR 20-NOV-2001; 2001US-0331647P.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX
XX Herath HMA, Parekh RB, Rohlf C;
XX
XX WPI; 2002-599812/64.
DR
XX
XX Screening or diagnosing multiple sclerosis (MS), useful for e.g.
PT determining the stage or severity of MS, comprises detecting the presence
PT of MS-associated features or protein isoforms by 2-dimensional
PT electrophoresis.
XX
XX
XX Disclosure; Page 32; 128pp; English.
PS
XX
XX This invention relates to a novel method for screening or diagnosing
CC

CC multiple sclerosis (MS) in a subject to determine the stage or severity
CC of MS, to identify a subject at risk of developing MS or to monitor the
CC effect of a therapy administered. The method comprises analysing a sample
CC body fluid from the subject by two-dimensional electrophoresis and
CC detecting the presence of multiple sclerosis-associated features (MSFs),
CC or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of
CC the invention correspond to spots identified on a 2D gel these proteins
CC may have antiinflammatory or neuroprotective activity. The methods of the
CC invention and the compositions are useful for clinical screening,
CC diagnosis and treatment of MS, for monitoring the effectiveness of MS
CC treatment, for selecting participants in clinical trials, for identifying
CC patients most likely to respond to a particular therapeutic treatment and
CC for screening and developing drugs for treatment of MS. Agents that
CC modulate the expression or activity of an MSPI are useful for treating
CC MS, for preventing or delaying the onset or development of MS, to prevent
CC or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic
CC acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,
CC or their fragments are useful for promoting MSPI function by gene
CC therapy. The present sequence represents a human multiple sclerosis
CC associated feature tryptic digest peptide of the invention
XX
SQ Sequence 16 AA:
Query Match 100.0%; Score 83; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADGSGDPLAEGGVR 16
Db 1 ADGSGDPLAEGGVR 16
|||||
RESULT 9
ABG70000
ID ABG70000 standard; peptide; 16 AA.
XX
AC ABG70000;
XX
DT 21-OCT-2002 (first entry)
XX
DE Antimicrobial peptide CS-FBPa.
XX
KM Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KM bacterial infection; fungal infection; fungicide; disinfectant;
KM preservative; foods; cosmetic; multiple antibiotic resistance.
XX
OS Unidentified.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001MO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 18; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The

CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is an antimicrobial peptide detailed in the
CC disclosure but specifically excluded from the scope of the invention
XX
SQ Sequence 16 AA:
Query Match 100.0%; Score 83; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADGSGDPLAEGGVR 16
Db 1 ADGSGDPLAEGGVR 16
|||||
RESULT 10
ABG69911
ID ABG69911 standard; peptide; 16 AA.
XX
AC ABG69911;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #23.
XX
KM Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KM bacterial infection; fungal infection; fungicide; disinfectant;
KM preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KM mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001MO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 135; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein) and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 CC
 SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADGEGDPLAEGGVR 16
 |||
 DB 1 ADGEGDPLAEGGVR 16

RESULT 11

ABP60019
 ID ABP60019 standard; peptide; 16 AA.

AC ABP60019;

XX 24-FEB-2003 (first entry)

XX Biopolymer disease specific marker.

XX Biopolymer; disease specific marker; myocardial infarction;
 KM alpha fibrinogen.

XX Homo sapiens.

XX WO200288716-A2.

XX 07-NOV-2002.

XX 25-APR-2002; 2002MO-CA000577.

XX 30-APR-2001; 2001US-00845765.

XX (SYN-) SYN X PHARMA INC.

XX Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;

XX WPI; 2003-111905/10.

XX New biopolymer marker or its analyte, useful for determining the presence
 PT or absence of at least one particular disease state, such as myocardial
 PT infarction.

XX Claim 1; Page 28; 28pp; English.

XX The invention relates to a biopolymer disease specific marker. The
 CC biopolymer marker is useful in indicating at least one particular disease
 CC state, such as myocardial infarction. The method is useful for evidencing
 CC and categorising at least one biopolymer marker sequence to determine the
 CC presence or absence of at least one disease state. This marker is
 CC characterised as an alpha fibrinogen having a molecular weight of 1518
 CC daltons. The current sequence represents the biopolymer disease specific
 CC marker of the invention

SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADGEGDPLAEGGVR 16
 |||
 DB 1 ADGEGDPLAEGGVR 16

RESULT 12

ABP60640
 ID ABP60640 standard; peptide; 16 AA.

AC ABP60640;

XX 28-MAR-2003 (first entry)

XX Fibrinopeptide A.

XX Fibrinopeptide A; N-terminus; protein identification.

XX Unidentified.

XX WO200295419-A2.

XX 28-NOV-2002.

XX 20-MAY-2002; 2002MO-US016247.

XX 23-MAY-2001; 2001US-00863786.

XX 20-DEC-2001; 2001US-0243019P.

XX (AMSH) AMERSHAM BIOSCIENCES AB.

XX (PROC) PROCTER & GAMBLE CO.

XX Bhikhabhai R, Liminga M, Maloised J, Palmgren R, Keough TW;

XX Youngquist RS, Vaughn HL, Yelm KE;

XX WPI; 2003-175111/17.

XX Identification of polypeptide useful in proteomics, involves
 PT derivatizing N-terminus or N-termini of polypeptide with acidic reagent
 PT containing sulfonyl or sulfonic acid moiety coupled to activated ester
 PT moiety.

XX Example 3; Page 29; 90pp; English.

XX The invention relates to a novel method for the identification of a
 CC polypeptide involving a step of derivatising the N-terminus of the
 CC polypeptide or the N-termini of one or more polypeptides with acidic
 CC reagent containing a sulfonyl or sulfonic acid moiety coupled to an
 CC activated ester moiety, analysing the derivative using mass spectrometry
 CC and interpreting the resulting fragmentation pattern. The present
 CC sequence represents Fibrinopeptide A, used in example 3 of the invention

SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16
| | | | | | | | | | | | | | | |
Db 1 ADSEGDPLAEGGVR 16

RESULT 13
ADA18542 standard; peptide; 16 AA.

ID ADA18542 standard; peptide; 16 AA.
AC ADA18542;
XX
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human alpha fibrinogen peptide #2.
DE
XX
XX Alpha fibrinogen; human; myocardial infarction; SELDI; mass spectrometry;
KM surfaces enhanced for laser desorption/ionisation.
XX
XX Homo sapiens.
OS
XX
XX US2002160423-A1.
PN
XX 31-OCT-2002.
PD
XX 30-APR-2001; 2001US-00846780.
PF
XX 30-APR-2001; 2001US-00846780.
PR
XX (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX
XX Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
PI
XX WPI; 2003-219987/21.
DR
XX
XX Biopolymer marker useful in indicating particular disease state
PT particularly myocardial infarction.
XX
XX Claim 1; Page 7; 10pp; English.

XX The invention relates to a biopolymer marker useful in indicating at
CC least one particular disease state. This marker is characterised as alpha
CC fibrinogen having a molecular weight of 1536 Daltons and is useful for
CC indicating a disease state, in particular myocardial infarction. The
CC marker sequences are useful as antigens in immunoassays for the detection
CC of those individuals suffering from the disease known to be evidenced by
CC the marker sequence. The marker provides an efficient diagnostic tool for
CC rapidly and accurately diagnosing disease states such as myocardial
CC infarction. The marker was detected by the technique of surfaces enhanced
CC for laser desorption/ionisation (SELDI) mass spectroscopy. The present
CC sequence is the alpha fibrinogen marker peptide.
XX
XX Sequence 16 AA;
SQ

Query Match 100.0%; Score 83; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16
| | | | | | | | | | | | | | | |
Db 1 ADSEGDPLAEGGVR 16

RESULT 14
ABR58740 standard; peptide; 16 AA.
ID ABR58740 standard; peptide; 16 AA.
XX
XX ABR58740;
AC

XX 11-JUL-2003 (first entry)
DT
XX Alzheimer's Disease-associated protein isoform, API-378, SEQ ID 8.
XX
DE
XX Neurotropic; Neuroprotective; Alzheimer's disease; API; human;
KM Alzheimer's Disease-associated protein isoform.
XX
XX Homo sapiens.
OS
XX
XX WO2003028543-A2.
PN
XX 10-APR-2003.
PD
XX 03-OCT-2002; 2002MO-US031642.
PF
XX 03-OCT-2001; 2001US-0326708P.
PR
XX (PF12) PFIZER PROD INC.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Durham UK, Friedman DL, Herath HMA, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stieger TR;
PI Sunderland PT, Townsend RR, White WF, Williams SA;
XX
XX WPI; 2003-371957/35.
DR
XX
XX Screening or diagnosing of Alzheimer's disease (AD) determine the stage
PT or severity of AD in a subject, comprises analyzing a test sample of body
PT fluid from the subject by 2-dimensional electrophoresis.
XX
XX Claim 2; Page 31; 179pp; English.

XX The present invention relates to methods for screening or diagnosing
CC Alzheimer's disease (AD) to determine the stage or severity of AD in a
CC subject, to identify subject at risk of developing AD, or to monitor the
CC effect of therapy administered. The methods comprise analyzing a test
CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-
CC dimensional array of AD-associated features (AFs). The method
CC alternatively comprises quantitatively detecting in a sample of body
CC fluid from the subject, one or more AD-associated protein isoforms (APIs;
CC ABR58710-ABR59184)
XX
XX Sequence 16 AA;
SQ

Query Match 100.0%; Score 83; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16
| | | | | | | | | | | | | | | |
Db 1 ADSEGDPLAEGGVR 16

RESULT 15
ADF51340 standard; peptide; 16 AA.
ID ADF51340 standard; peptide; 16 AA.
XX
XX ADF51340;
AC
XX 12-FEB-2004 (first entry)
DT
XX
XX Antiangiogenic fibrinogen derived peptide 66.
DE
XX
XX fibrinogen; antiangiogenic; cytostatic; angiogenesis; gene therapy;
KM cancer; human; mutant; mutlein.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "N-terminal acetyl"

```

FT Modified-site 16
FT /note= "C-terminal amide"
XX
XX
PN WO2003070769-A2.
XX
XX
PD 28-AUG-2003.
XX
PF 19-FEB-2003; 2003WO-EP001698.
XX
PR 19-FEB-2002; 2002GB-00003882.
PR 19-FEB-2002; 2002GB-00003883.
PR 23-JUL-2002; 2002GB-00017067.
XX
XX (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS PHARMA GMBH.
PA (BIOA-) BIOACTA LTD.
XX
XX
PI Garcia-Echeverria C, Lewis C, Robinson J;
DR WPI; 2003-731548/69.
XX
XX
PT New polypeptide derived from fibrinogen and having anti-angiogenic
XX activity, useful for preparing a composition for treating cancer.
XX
PS Example 37; Fig 3; 66pp; English.
XX
XX This invention relates to a novel polypeptide derived from fibrinogen
CC comprising 15 or less amino acids which has antiangiogenic activity. The
CC invention may be useful for the development of compounds with a
CC cytostatic activity through the inhibition of angiogenesis. The sequences
CC of the invention may be useful for gene therapy. The polypeptide is
CC useful for inhibiting angiogenesis and in preparing a composition for
XX treating cancer.
XX
SQ Sequence 16 AA;

```

```

Query Match 100.0%; Score 83; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ADSGEGDFLAEGGVR 16
   |||||
Db 1 ADSGEGDFLAEGGVR 16

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Search completed: January 21, 2005, 08:31:10
 Job time : 88 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 26 Seconds
(without alignments)
40.811 Million cell updates/sec

Title: US-09-845-765-1
Sequence: 1 ADSCGDFLAEGGCV 16

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	16	2	US-08-796-598-14
2	83	100.0	16	2	US-08-447-175A-14
3	83	100.0	16	3	US-08-469-141A-56
4	83	100.0	16	4	US-09-525-269A-25
5	83	100.0	16	5	PCT-US95-13794-56
6	83	100.0	17	4	US-09-845-719B-1
7	83	100.0	18	3	US-08-469-141A-55
8	83	100.0	18	5	PCT-US95-13794-55
9	83	100.0	19	3	US-08-469-141A-54
10	83	100.0	19	5	PCT-US95-13794-54
11	83	100.0	20	1	US-08-288-657-1
12	83	100.0	20	1	US-07-984-884-1
13	83	100.0	20	1	US-08-481-810-1
14	83	100.0	20	1	US-08-484-426-1
15	83	100.0	20	2	US-08-480-818-1
16	83	100.0	20	3	US-08-469-141A-53
17	83	100.0	20	4	US-09-525-269A-26
18	83	100.0	20	5	PCT-US95-13794-53
19	83	100.0	21	3	US-08-469-141A-45
20	83	100.0	21	5	PCT-US95-13794-45
21	83	100.0	22	3	US-08-469-141A-44
22	83	100.0	22	3	US-08-469-141A-52
23	83	100.0	22	5	PCT-US95-13794-44
24	83	100.0	22	5	PCT-US95-13794-52
25	83	100.0	25	3	US-08-860-808E-25
26	83	100.0	25	3	US-08-440-332-16
27	83	100.0	25	3	US-08-440-331-16

28	83	100.0	30	2	US-07-963-538B-9	Sequence 9, Appli
29	83	100.0	643	2	US-08-551-356-4	Sequence 4, Appli
30	83	100.0	643	5	PCT-US93-12687-4	Sequence 4, Appli
31	83	100.0	644	1	US-08-206-176-2	Sequence 2, Appli
32	83	100.0	644	4	US-09-919-039-121	Sequence 121, App
33	83	100.0	847	4	US-09-373-157-4	Sequence 4, Appli
34	69	83.1	14	4	US-09-845-725A-1	Sequence 1, Appli
35	63	75.9	17	3	US-08-469-141A-46	Sequence 46, Appli
36	63	75.9	17	5	PCT-US95-13794-46	Sequence 46, Appli
37	58	69.9	12	4	US-09-846-350A-1	Sequence 1, Appli
38	58	69.9	28	6	5196404-16	Patent No. 5196404
39	53	63.9	10	6	5196404-18	Patent No. 5196404
40	53	63.9	10	6	5433940-25	Patent No. 5433940
41	52	62.7	15	3	US-08-469-141A-6	Sequence 6, Appli
42	52	62.7	15	5	PCT-US95-13794-6	Sequence 6, Appli
43	52	62.7	24	2	US-08-978-404B-48	Sequence 48, Appli
44	46	55.4	17	2	US-08-792-553-11	Sequence 11, Appli
45	46	55.4	17	4	US-09-129-192C-45	Sequence 45, Appli

ALIGNMENTS

RESULT 1
US-08-796-598-14
; Sequence 14, Application US/08796598
; Patent No. 5827659

GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.

TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESS: Thibault
STREET: High Street Tower, 125 High Street

CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,598

FILING DATE: 07-FEB-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,055

FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: FLYNN Bq., Kerry A.

REGISTRATION NUMBER: 33,693

REFERENCE/DOCKET NUMBER: SYP-115

TELEPHONE: (617) 248-7100

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-796-598-14

Query Match 100.0%; Score 83; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3; De-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSEGDPLAEGGVR 16
|||
Db 1 ADSEGDPLAEGGVR 16

RESULT 2

US-08-447-175A-14
Sequence 14, Application US/08447175A
Patent No. 5869240
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
SPECTROMETRY.
TITLE OF INVENTION: 23
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,175A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: RAUSCHENBACH, Kurt
REGISTRATION NUMBER: 40,137
REFERENCE/DOCKET NUMBER: SYP-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-447-175A-14

Query Match 100.0%; Score 83; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSEGDPLAEGGVR 16
|||
Db 1 ADSEGDPLAEGGVR 16

RESULT 3

US-08-469-141A-56
Sequence 56, Application US/08469141A
Patent No. 6124107
GENERAL INFORMATION:
APPLICANT: MUMFORD, RICHARD A.
APPLICANT: DAVIES, D.T. PHILIP
APPLICANT: DAHLGREN, MARY E.
APPLICANT: BOGER, JOSHUA S.
APPLICANT: HOMES, JOHN L.
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: DR. CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000

CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,141A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 174611B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-6734
TELEFAX: (908)-594-4720
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-469-141A-56

Query Match 100.0%; Score 83; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSEGDPLAEGGVR 16
|||
Db 1 ADSEGDPLAEGGVR 16

RESULT 4

US-09-525-269A-25
Sequence 25, Application US/09525269A
Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
Peptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 16
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antimicrobial peptide designed in part upon
microbial domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-25

Query Match 100.0%; Score 83; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSEGDPLAEGGVR 16
|||

Db 1 ADGSGDPLAEGGVR 16

RESULT 5

PCT-US95-13794-56
 ; Sequence 56, Application PC/TUS9513794
 ; GENERAL INFORMATION:
 ; APPLICANT: Mumford, Richard A.
 ; APPLICANT: Davies, D.T., Philip
 ; APPLICANT: Dahlgren, Mary E.
 ; APPLICANT: Boger, Joshua S.
 ; APPLICANT: Humes, John L.
 ; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
 ; TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dr. Christine E. Carly
 ; STREET: 126 E. Lincoln Avenue, P.O. Box 2000
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07065-0907
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13794
 ; FILING DATE: 03-NOV-1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Carly, Christine E.
 ; REGISTRATION NUMBER: 36,099
 ; REFERENCE/DOCKET NUMBER: 174611AY
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 594-6734
 ; TELEFAX: (908) 594-4720
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; PCT-US95-13794-56

Query Match 100.0%; Score 83; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3, 8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADGSGDPLAEGGVR 16
 |||||
 Db 1 ADGSGDPLAEGGVR 16

RESULT 6

US-09-845-719B-1
 ; Sequence 1, Application US/09845719B
 ; Patent No. 6627606
 ; GENERAL INFORMATION:
 ; APPLICANT: JACOBOWSKI, George
 ; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
 ; FILE REFERENCE: 2132, 035
 ; CURRENT APPLICATION NUMBER: US/09/845,719B
 ; CURRENT FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 1

; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-845-719B-1

Query Match 100.0%; Score 83; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADGSGDPLAEGGVR 16
 |||||
 Db 1 ADGSGDPLAEGGVR 16

RESULT 7

US-08-469-141A-55
 ; Sequence 55, Application US/08469141A
 ; Patent No. 6124107
 ; GENERAL INFORMATION:
 ; APPLICANT: MUMFORD, RICHARD A.
 ; APPLICANT: DAVIES, D.T., PHILIP
 ; APPLICANT: DAHLGREN, MARY E.
 ; APPLICANT: BOGER, JOSHUA S.
 ; APPLICANT: HUMES, JOHN L.
 ; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
 ; TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DR. CHRISTINE E. CARLY
 ; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07065-0907
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/469,141A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CARLY, CHRISTINE E.
 ; REGISTRATION NUMBER: 36,099
 ; REFERENCE/DOCKET NUMBER: 174611B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908)-594-6734
 ; TELEFAX: (908)-594-4720
 ; INFORMATION FOR SEQ ID NO: 55:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; US-08-469-141A-55

Query Match 100.0%; Score 83; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4, 3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADGSGDPLAEGGVR 16
 |||||
 Db 1 ADGSGDPLAEGGVR 16

RESULT 8
 PCT-US95-13794-55

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/ Sequence 55, Application PC/TUS9513794
/ GENERAL INFORMATION:
/ APPLICANT: Mumford, Richard A.
/ APPLICANT: Davies, D.T. Philip
/ APPLICANT: Dahlgren, Mary E.
/ APPLICANT: Boger, Joshua S.
/ APPLICANT: Humes, John L.
/ TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
/ TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
/ NUMBER OF SEQUENCES: 71
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dr. Christine E. Carly
/ STREET: 126 E. Lincoln Avenue, P.O. Box 2000
/ CITY: Rahway
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07065-0907
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/13794
/ FILING DATE: 03-NOV-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Carly, Christine E.
/ REGISTRATION NUMBER: 36,099
/ REFERENCE/DOCKET NUMBER: 174611AY
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 594-6734
/ TELEFAX: (908) 594-4720
/ INFORMATION FOR SEQ ID NO: 55:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ PCT-US95-13794-55

Query Match 100.0%; Score 83; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. NO. 4.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ADSEGDPLAEGGVR 16
Db 1 ADSEGDPLAEGGVR 16

RESULT 9
US-08-469-141A-54
/ Sequence 54, Application US/08469141A
/ Patent No. 6124107
/ GENERAL INFORMATION:
/ APPLICANT: Mumford, Richard A.
/ APPLICANT: Davies, D.T. Philip
/ APPLICANT: Dahlgren, Mary E.
/ APPLICANT: Boger, Joshua S.
/ APPLICANT: Humes, John L.
/ TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
/ TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
/ NUMBER OF SEQUENCES: 71
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dr. Christine E. Carly
/ STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
/ CITY: RAHWAY
/ STATE: NEW JERSEY
/ COUNTRY: USA
```

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/ ZIP: 07065-0907
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/469,141A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CARLY, CHRISTINE E.
/ REGISTRATION NUMBER: 36,099
/ REFERENCE/DOCKET NUMBER: 174611B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) -594-6734
/ TELEFAX: (908) -594-4720
/ INFORMATION FOR SEQ ID NO: 54:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ US-08-469-141A-54

Query Match 100.0%; Score 83; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ADSEGDPLAEGGVR 16
Db 1 ADSEGDPLAEGGVR 16

RESULT 10
PCT-US95-13794-54
/ Sequence 54, Application PC/TUS9513794
/ GENERAL INFORMATION:
/ APPLICANT: Mumford, Richard A.
/ APPLICANT: Davies, D.T. Philip
/ APPLICANT: Dahlgren, Mary E.
/ APPLICANT: Boger, Joshua S.
/ APPLICANT: Humes, John L.
/ TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
/ TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
/ NUMBER OF SEQUENCES: 71
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dr. Christine E. Carly
/ STREET: 126 E. Lincoln Avenue, P.O. Box 2000
/ CITY: Rahway
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07065-0907
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/13794
/ FILING DATE: 03-NOV-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Carly, Christine E.
/ REGISTRATION NUMBER: 36,099
/ REFERENCE/DOCKET NUMBER: 174611AY
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 594-6734
/ TELEFAX: (908) 594-4720
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OTHER INFORMATION: thrombin cleavage site in the human fibrinogen
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; FEATURE: Cleavage-site
; NAME/KEY:
; LOCATION: 16..17
US-08-288-657-1

Query Match 100.0%; Score 83; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 4.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADGSGDPLAEGGVR 16
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1 ADGSGDPLAEGGVR 16
|||
Db 1 ADGSGDPLAEGGVR 16
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RESULT 12
US-07-984-884-1
; Sequence 1, Application US/07984884
; Patent No. 5614499
; GENERAL INFORMATION:
; APPLICANT: Teger-Nilsson, Ann-Catrine E
; APPLICANT: Bylund, Ruth E
; TITLE OF INVENTION: New peptide derivatives
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White and Case
; STREET: 115 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/984,884
; FILING DATE: 02-DEC-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J
; REGISTRATION NUMBER: 35, 372
; REFERENCE/DOCKET NUMBER: 1103326-016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8200
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-07-984-884-1

Query Match 100.0%; Score 83; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 4.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADGSGDPLAEGGVR 16
|||
1 ADGSGDPLAEGGVR 16
|||
Db 1 ADGSGDPLAEGGVR 16

RESULT 13
US-08-481-810-1
; Sequence 1, Application US/08481810
; Patent No. 5736521
; GENERAL INFORMATION:
; APPLICANT: Teger-Nilsson, Ann-Catrine E

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APPLICANT: Bylund, Ruth E
TITLE OF INVENTION: New peptide derivatives
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,810
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984884
FILING DATE: 02-DEC-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-481-810-1

Query Match 100.0%; Score 83; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSEGDPLAEGGVR 16
Db 1 ADSEGDPLAEGGVR 16

RESULT 14
US-08-484-426-1
Sequence 1, Application US/08484426
Patent No. 5747460
GENERAL INFORMATION:
APPLICANT: Teger-Nilsson, Ann-Catrine E
APPLICANT: Bylund, Ruth E
TITLE OF INVENTION: New peptide derivatives
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,426
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984884
FILING DATE: 02-DEC-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-484-426-1

Query Match 100.0%; Score 83; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSEGDPLAEGGVR 16
Db 1 ADSEGDPLAEGGVR 16

RESULT 15
US-08-480-818-1
Sequence 1, Application US/08480818
Patent No. 5955433
GENERAL INFORMATION:
APPLICANT: Teger-Nilsson, Ann-Catrine E
APPLICANT: Bylund, Ruth E
TITLE OF INVENTION: New peptide derivatives
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,818
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984884
FILING DATE: 02-DEC-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-480-818-1

Query Match 100.0%; Score 83; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ADGSGDPLAEGGVR 16

Search completed: January 21, 2005, 08:29:37
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:53 ; Search time 75 Seconds
(without alignments)
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Title: US-09-845-765-1
Perfect score: 83
Sequence: 1 ADSCGDFLAEGGVR 16

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_MA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	16	9 US-09-846-780-1	Sequence 1, Appl1
2	83	100.0	16	9 US-09-826-290-352	Sequence 352, Appl1
3	83	100.0	16	12 US-09-845-765-1	Sequence 1, Appl1
4	83	100.0	16	14 US-10-359-363A-2	Sequence 2, Appl1
5	83	100.0	16	15 US-10-264-309-8	Sequence 8, Appl1
6	83	100.0	16	16 US-10-325-162-1	Sequence 1, Appl1
7	83	100.0	16	17 US-10-484-568-60	Sequence 60, Appl1
8	83	100.0	17	14 US-10-197-954-53	Sequence 53, Appl1
9	83	100.0	24	15 US-10-363-369-3	Sequence 3, Appl1
10	83	100.0	24	15 US-10-363-369-4	Sequence 4, Appl1
11	83	100.0	24	15 US-10-363-369-5	Sequence 5, Appl1
12	83	100.0	24	15 US-10-363-369-6	Sequence 6, Appl1
13	83	100.0	24	17 US-10-484-568-1	Sequence 1, Appl1

14	83	100.0	24	17 US-10-484-568-3	Sequence 3, Appl1
15	83	100.0	24	17 US-10-484-568-10	Sequence 10, Appl1
16	83	100.0	24	17 US-10-484-568-25	Sequence 25, Appl1
17	83	100.0	24	17 US-10-484-568-40	Sequence 40, Appl1
18	83	100.0	24	17 US-10-484-568-41	Sequence 41, Appl1
19	83	100.0	24	17 US-10-484-568-42	Sequence 42, Appl1
20	83	100.0	24	17 US-10-484-568-43	Sequence 43, Appl1
21	83	100.0	24	17 US-10-484-568-44	Sequence 44, Appl1
22	83	100.0	24	17 US-10-484-568-45	Sequence 45, Appl1
23	83	100.0	24	17 US-10-484-568-46	Sequence 46, Appl1
24	83	100.0	24	17 US-10-484-568-47	Sequence 47, Appl1
25	83	100.0	24	17 US-10-484-568-48	Sequence 48, Appl1
26	83	100.0	24	17 US-10-484-568-49	Sequence 49, Appl1
27	83	100.0	25	9 US-09-757-774-16	Sequence 16, Appl1
28	83	100.0	28	17 US-10-484-568-61	Sequence 61, Appl1
29	83	100.0	28	17 US-10-484-568-62	Sequence 62, Appl1
30	83	100.0	78	15 US-10-363-369-15	Sequence 15, Appl1
31	83	100.0	360	9 US-09-925-297-587	Sequence 587, Appl1
32	83	100.0	388	15 US-10-336-392-34	Sequence 34, Appl1
33	83	100.0	481	15 US-10-336-392-36	Sequence 36, Appl1
34	83	100.0	620	10 US-09-931-009A-1	Sequence 1, Appl1
35	83	100.0	644	10 US-09-919-039-121	Sequence 121, Appl1
36	83	100.0	644	15 US-10-336-392-32	Sequence 32, Appl1
37	83	100.0	847	13 US-10-112-527-4	Sequence 4, Appl1
38	80	96.4	16	14 US-10-359-363A-25	Sequence 25, Appl1
39	80	96.4	24	17 US-10-484-568-27	Sequence 27, Appl1
40	79	95.2	15	9 US-09-845-719A-1	Sequence 1, Appl1
41	79	95.2	15	17 US-10-484-568-51	Sequence 51, Appl1
42	79	95.2	23	17 US-10-484-568-53	Sequence 53, Appl1
43	79	95.2	24	17 US-10-484-568-38	Sequence 38, Appl1
44	78	94.0	15	17 US-10-484-568-50	Sequence 50, Appl1
45	78	94.0	24	15 US-10-363-369-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-846-780-1
Sequence 1, Application US/09846780
Patent No. US20020160423A1
GENERAL INFORMATION:
APPLICANT: JACOBOWSKI, GEORGE
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1536 DALTONS
FILE REFERENCE: 2132.039
CURRENT APPLICATION NUMBER: US/09/846,780
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-846-780-1

Query Match 100.0%; Score 83; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSCGDFLAEGGVR 16
Db 1 ADSCGDFLAEGGVR 16

RESULT 2
US-09-826-290-352
Sequence 352, Application US/09826290
Patent No. US20020164668A1
GENERAL INFORMATION:
APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI

APPLICANT: Kimmel, Lida H.
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Potter, David M.
APPLICANT: Rohlf, Christian
APPLICANT: Silber, B. Michael
APPLICANT: Stigter, Thomas R.
APPLICANT: Sunderland, P. Trey
APPLICANT: Townsend, Robert Reid
APPLICANT: Williams, Stephen A.
APPLICANT: White, Frost
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 2572-1-001 N2
CURRENT APPLICATION NUMBER: US/09/826,290
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 352
LENGTH: 16
TYPE: PRT
ORGANISM: homo sapien
US-09-826-290-352

Query Match 100.0%; Score 83; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADGSGDFLAEGGVR 16
Db 1 ADGSGDFLAEGGVR 16

RESULT 3
US-09-845-765-1
Sequence 1, Application US/09845765
Publication No. US20040198950A1
GENERAL INFORMATION:
APPLICANT: JACKOWSKI, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
FILE REFERENCE: 2132.036
CURRENT APPLICATION NUMBER: US/09/845,765
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-845-765-1

Query Match 100.0%; Score 83; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADGSGDFLAEGGVR 16
Db 1 ADGSGDFLAEGGVR 16

RESULT 4
US-10-359-363A-2
Sequence 2, Application US/10359363A
Publication No. US20030228371A1
GENERAL INFORMATION:
APPLICANT: Skinner, James E.
APPLICANT: Anchin, Jerry M.
TITLE OF INVENTION: ANTI-INFARCTION MOLECULES

FILE REFERENCE: 22118.0001U4
CURRENT APPLICATION NUMBER: US/10/359,363A
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: 60/429,278
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: 60/392,133
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/354,678
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1 =
US-10-359-363A-2

Query Match 100.0%; Score 83; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADGSGDFLAEGGVR 16
Db 1 ADGSGDFLAEGGVR 16

RESULT 5
US-10-264-309-8
Sequence 8, Application US/10264309
Publication No. US20040022794A1
GENERAL INFORMATION:
APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH
APPLICANT: KIMMEL, LIDA H.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: POTTER, DAVID M.
APPLICANT: ROHLF, CHRISTIAN
APPLICANT: SILBER, B. MICHAEL
APPLICANT: SNYDER, PETER J.
APPLICANT: SOARES, HOLLY D.
APPLICANT: STIGTER, THOMAS R.
APPLICANT: SUNDERLAND, P. TREY
APPLICANT: TOWNSEND, ROBERT R.
APPLICANT: WHITE, W. FROST
APPLICANT: WILLIAMS, STEPHEN A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn version 2.1
SEQ ID NO 8
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-309-8

Query Match 100.0%; Score 83; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADGSGDFLAEGGVR 16
Db 1 ADGSGDFLAEGGVR 16

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RESULT 6
US-10-325-162-1
; Sequence 1, Application US/10325162
; Publication NO. US20040121306A1
; GENERAL INFORMATION:
; APPLICANT: Kupchak, Peter
; APPLICANT: Marshall, John
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Method of Confirming the Presence of Myocardial Infarction
; FILE REFERENCE: 2132.132
; CURRENT APPLICATION NUMBER: US/10/325.162
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-325-162-1

Query Match      100.0%; Score 83; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDPLAEGGVR 16
DB      1 ADSGEGDPLAEGGVR 16

RESULT 7
US-10-484-568-60
; Sequence 60, Application US/10484568
; Publication NO. US20040248194A1
; GENERAL INFORMATION:
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Lewis, Claire
; APPLICANT: Robinson, Jeffrey
; TITLE OF INVENTION: Peptide Screen
; FILE REFERENCE: 4-32520A/32360/361
; CURRENT APPLICATION NUMBER: US/10/484.568
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-484-568-60

Query Match      100.0%; Score 83; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDPLAEGGVR 16
DB      1 ADSGEGDPLAEGGVR 16

RESULT 8
US-10-197-954-53
; Sequence 53, Application US/10197954
; Publication NO. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqui, Suhailb
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197.954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
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; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-53

Query Match      100.0%; Score 83; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDPLAEGGVR 16
DB      2 ADSGEGDPLAEGGVR 17

RESULT 9
US-10-363-369-3
; Sequence 3, Application US/10363369
; Publication NO. US20040039157A1
; GENERAL INFORMATION:
; APPLICANT: Biocarta Limited
; TITLE OF INVENTION: Anti-Angiogenic Peptides
; FILE REFERENCE: P38123WO
; CURRENT APPLICATION NUMBER: US/10/363.369
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: 0021475.9
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-369-3

Query Match      100.0%; Score 83; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDPLAEGGVR 16
DB      1 ADSGEGDPLAEGGVR 16

RESULT 10
US-10-363-369-4
; Sequence 4, Application US/10363369
; Publication NO. US20040039157A1
; GENERAL INFORMATION:
; APPLICANT: Biocarta Limited
; TITLE OF INVENTION: Anti-Angiogenic Peptides
; FILE REFERENCE: P38123WO
; CURRENT APPLICATION NUMBER: US/10/363.369
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: 0021475.9
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (23)..(23)
; OTHER INFORMATION: any amino acid residue
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US-10-363-369-4

Query Match 100.0%; Score 83; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16
DB 1 ADSEGDPLAEGGVR 16

RESULT 11

US-10-363-369-5
; Sequence 5, Application US/10363369
; Publication No. US20040039157A1
; GENERAL INFORMATION:
; APPLICANT: Biocata Limited
; TITLE OF INVENTION: Anti-Angiogenic Peptides
; FILE REFERENCE: P38123WO
; CURRENT APPLICATION NUMBER: US/10/363,369
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: 0021475.9
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (19)..(19)
; OTHER INFORMATION: any amino acid residue
US-10-363-369-5

Query Match 100.0%; Score 83; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16
DB 1 ADSEGDPLAEGGVR 16

RESULT 12

US-10-363-369-6
; Sequence 6, Application US/10363369
; Publication No. US20040039157A1
; GENERAL INFORMATION:
; APPLICANT: Biocata Limited
; TITLE OF INVENTION: Anti-Angiogenic Peptides
; FILE REFERENCE: P38123WO
; CURRENT APPLICATION NUMBER: US/10/363,369
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: 0021475.9
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)..(17)
; OTHER INFORMATION: any amino acid residue
US-10-363-369-6

Query Match 100.0%; Score 83; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16

DB 1 ADSEGDPLAEGGVR 16

RESULT 13

US-10-484-568-1
; Sequence 1, Application US/10484568
; Publication No. US20040248194A1
; GENERAL INFORMATION:
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Lewis, Claire
; TITLE OF INVENTION: Peptide Screen
; FILE REFERENCE: 4-32520A/32360/361
; CURRENT APPLICATION NUMBER: US/10/484,568
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-484-568-1

Query Match 100.0%; Score 83; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16
DB 1 ADSEGDPLAEGGVR 16

RESULT 14

US-10-484-568-3
; Sequence 3, Application US/10484568
; Publication No. US20040248194A1
; GENERAL INFORMATION:
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Lewis, Claire
; APPLICANT: Robinson, Jeffrey
; TITLE OF INVENTION: Peptide Screen
; FILE REFERENCE: 4-32520A/32360/361
; CURRENT APPLICATION NUMBER: US/10/484,568
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (23)..(23)
; OTHER INFORMATION:
; NAME/KEY: MISC_FEATURE
; LOCATION: (23)..(23)
; OTHER INFORMATION: X = any amino acid
US-10-484-568-3

Query Match 100.0%; Score 83; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16
DB 1 ADSEGDPLAEGGVR 16

RESULT 15

US-10-484-568-10
; Sequence 10, Application US/10484568

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; Publication No. US20040248194A1
; GENERAL INFORMATION:
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Lewis, Claire
; APPLICANT: Robinson, Jeffrey
; TITLE OF INVENTION: Peptide Screen
; FILE REFERENCE: 4-32520A/32360/361
; CURRENT APPLICATION NUMBER: US/10/484,568
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: X = any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (22)-(22)
; OTHER INFORMATION: X = any amino acid
; US-10-484-568-10

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Query Match          100.0%; Score 83; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 2,7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ADGSGDPLAEGGVR 16
      |||||
Db      1 ADGSGDPLAEGGVR 16

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Search completed: January 21, 2005, 08:34:36
 Job time : 76 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 23 Seconds
(without alignments)
66,933 Million cell updates/sec

Title: US-09-845-765-1

Sequence: 1 ADGGEDEFLAEGGCV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.*
2: PIR1.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	644	1 FGHUA	fibrinogen alpha c
2	83	100.0	866	2 D44234	fibrinogen alpha c
3	80	96.4	16	2 A29501	fibrinopeptide A -
4	80	96.4	16	2 B24180	fibrinogen alpha c
5	80	96.4	16	2 A24180	fibrinogen alpha c
6	80	96.4	16	2 B28854	fibrinopeptide A -
7	80	96.4	16	2 C28854	fibrinopeptide A -
8	80	96.4	16	2 A28854	fibrinopeptide A -
9	62	74.7	16	2 H29501	fibrinopeptide A -
10	61	73.5	16	2 G29501	fibrinopeptide A -
11	60	72.3	28	2 A05296	fibrinogen alpha c
12	58	69.9	19	2 B29501	fibrinopeptide A -
13	58	69.9	311	2 A05294	fibrinogen alpha c
14	57	68.7	15	2 F29501	fibrinopeptide A -
15	55	66.3	17	2 E29501	fibrinopeptide A -
16	55	66.3	19	2 C29501	fibrinopeptide A -
17	54	65.1	15	2 I29501	fibrinopeptide A -
18	46	55.4	223	2 B96506	hypothetical prote
19	44	53.0	169	2 G83075	type 4 fibrinogen
20	44	53.0	274	2 G72685	probable alanyl-tr
21	44	53.0	669	2 A72718	hypothetical prote
22	43	51.8	278	2 S25355	hypothetical prote
23	43	51.8	692	1 S57592	probable phospho
24	42.5	51.2	518	2 A13534	probable binding p
25	42	50.6	15	2 U70101	fibrinogen alpha c
26	42	50.6	144	2 H84434	probable phloem-sp
27	42	50.6	168	2 T07146	pathogenesis-relat
28	42	50.6	602	1 GBPT4	gene 10 protein -
29	42	50.6	629	2 B75330	probable ribosomal

30	42	50.6	787	2 A44452	translatation initia
31	42	50.6	828	2 G87584	hypothetical prote
32	42	50.6	1024	2 S10056	hemolysin A - Esch
33	41	49.4	21	2 S47200	T-cell receptor J-
34	41	49.4	159	1 VCT014	pathogenesis-relat
35	41	49.4	159	1 S26238	pathogenesis-relat
36	41	49.4	236	2 S48867	dimethylallyltans
37	41	49.4	254	2 S30742	hypothetical prote
38	41	49.4	254	2 D86068	hypothetical prote
39	41	49.4	254	2 A91232	hypothetical prote
40	41	49.4	284	2 A97203	2-oxoacid ferredox
41	41	49.4	391	2 T36321	hypothetical prote
42	41	49.4	394	2 AG3616	hypothetical prote
43	41	49.4	399	2 A87392	conserved hypothet
44	41	49.4	425	2 AG2787	long-chain fatty a
45	41	49.4	429	2 A97567	hypothetical prote

ALIGNMENTS

RESULT 1

FGHUA

fibrinogen alpha chain precursor, short splice form [validated] - human

N/Alternate names: coagulation factor I

N/Contains: fibrinopeptide A

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 30-Jun-1987 #text change 09-Jul-2004

C/Accession: A93956; A43568; A90468; 184456; A44234; C44234; B94433; A90433; B94309; S19

R/Kant, J.A.; Lord, S.T.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983

A/Title: Partial mRNA sequences for human Aa1pha, Bbeta, and gamma fibrinogen chains: ev

A/Reference number: A93956; MUID:83247396; PMID:6575389

A/Accession: A93956

A/Molecule type: mRNA

A/Residues: 1-644 <KAN>

A/Cross-references: UNIPROT:P02671; GB:J00128; NID:G182425; PIDN:AA52426.1; PID:G182426

A/Note: the authors translated the codon GAG for residue 247 as Gly, GGA for residue 438

A/Title: Nucleotide sequences of the three genes coding for human fibrinogen.

A/Reference number: A43568; MUID:91344740; PMID:2102623

A/Accession: A43568

A/Molecule type: DNA

A/Residues: 1-330, 'A', 332-644 <CHU>

A/Cross-references: GB:M64982; NID:G458553; PIDN:AA17055.1; PID:G458554

R/Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.

Biochemistry 22, 3237-3244, 1983

A/Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha c

A/Reference number: A90468; MUID:83283432; PMID:6688355

A/Accession: A90468

A/Molecule type: mRNA

A/Residues: 1-330, 'A', 332-629 <RIX>

A/Cross-references: GB:J00127; NID:G182423; PIDN:AA52426.1; PID:G182424

R/Riman, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.

Nucleic Acids Res. 11, 7427-7434, 1983

A/Title: Isolation and characterisation of cDNA clones for the alpha- and gamma-chains c

A/Reference number: I37393; MUID:84069777; PMID:6689067

A/Accession: 184456

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 110-156 <RES>

A/Cross-references: GB:K02272; NID:G182427; PIDN:AA52428.1; PID:G182428

R/Fu, Y.; Weisbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redmar

Biochemistry 31, 11968-11972, 1992

A/Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove

A/Reference number: A44234; MUID:93090725; PMID:1457396

A/Accession: A44234

A/Molecule type: mRNA

A/Residues: 1-51 <FUI>

A/Cross-references: GB:M64982; NID:G458553; PIDN:AA17055.1; PID:G458554

A/Note: sequence extracted from NCBI backbone (NCBIN:119912, NCBIN:119914, NCBI:119918)

A/Accession: C44234

A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 605-644 <FU2>
 A:Cross-references: GB:M64982; NID:G458553; PID:AAA17055.1; PID:G458554
 A>Note: sequence extracted from NCBI backbone (NCBI:119920)
 R:Henschel, A.; Lottepeich, F.; Southan, C.; Topfer-Petersen, E.
 in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
 A>Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
 A:Reference number: A94433
 A:Accession: B94303
 A:Molecule type: protein
 A:Residues: 20-214, 'RS', 217-298, 'G', 300-303, 'G', 305-629 <HEN>
 R:Walt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
 Biochemistry 18, 5410-5416, 1979
 A>Title: Amino acid sequences studies on the alpha chain of human fibrinogen. Overlappi
 A:Reference number: A90433; MUID:80088231; PMID:518846
 A:Contents: disulfide bonds
 A:Accession: A90433
 A:Molecule type: protein
 A:Residues: 20-146, 'Q', 148-195, 'N', 197-230, 'N', 232-316, 'SG', 319-406, 'D', 408, 'N', 410-629
 R:Blomback, B.; Hessel, B.; Hog9, D.
 Thromb. Res. 8, 639-658, 1976
 A>Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
 A:Reference number: A94309; MUID:7625080; PMID:936108
 A:Contents: variant, and disulfide bonds
 A:Accession: B94309
 A:Molecule type: protein
 A:Residues: 20-65, 'T', 67-629 <BLO>
 R:Dewey, R.S.; Liesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumfor
 Biochem. J. 281, 519-524, 1992
 A>Title: Purification and characterization by fast-atom-bombardment mass spectrometry of
 incubation with calcium ionophore A23187.
 A:Reference number: S19297; MUID:92143822; PMID:1736899
 A:Accession: S19297
 A:Molecule type: protein
 A:Residues: 20-40 <DEW>
 R:Retzius, A.D.; Markland Jr., F.S.
 Thromb. Res. 52, 541-552, 1988
 A>Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co
 A:Reference number: A60905; MUID:89162316; PMID:3232124
 A:Accession: A60905
 A:Molecule type: protein
 A:Residues: 433-451 <RET>
 R:Retzius, A.D.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
 J. Biol. Chem. 253, 2184-2195, 1978
 A>Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
 A:Reference number: A92225; MUID:79130085; PMID:632262
 A:Contents: annotation; cross-linking acceptor sites
 R:Cottrell, B.A.; Strong, D.D.; Walt, K.W.K.; Doolittle, R.F.
 Biochemistry 18, 5405-5410, 1979
 A>Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locat
 A:Reference number: A90432; MUID:80088230; PMID:518845
 A:Contents: annotation; cross-linking acceptor sites
 R:Henschel, A.; Lottepeich, F.; Kehl, M.; Southan, C.
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983
 A>Title: Covalent structure of fibrinogen.
 A:Reference number: A90037; MUID:83254370; PMID:6575689
 A:Contents: annotation; review, disulfide bonds
 R:Tarate, E.; Plana, M.; Guasch, M.D.; Marcos, C.
 Biochem. Biophys. Res. Commun. 117, 631-636, 1983
 A>Title: Phosphorylation of fibrinogen by casein kinase 1.
 A:Reference number: A90116; MUID:84104274; PMID:6318767
 A:Contents: annotation; phosphorylation
 A>Note: about one-third of alpha chain molecules in blood were found to be phosphorylate
 R:Doolittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A>Title: Fibrinogen and fibrin.
 A:Reference number: A90041; MUID:84305751; PMID:6383194
 A:Contents: annotation; review, EM structure, polymerization, ligands
 R:Kimura, S.; Aoki, N.
 J. Biol. Chem. 261, 15591-15595, 1986
 A>Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
 A:Reference number: A92565; MUID:87057190; PMID:2877981

A:Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
 R:Krishnamurthi, S.; Dickens, T.A.; Patel, Y.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
 Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
 A>Title: The fibrinogen-derived peptide (RGSS) prevents proteolytic degradation of protei
 A:Reference number: A33261; MUID:89392031; PMID:2783116
 A:Contents: annotation; activity of cell attachment (R-G-D) motif
 R:Kirschbaum, N.E.; Budeynski, A.G.
 J. Biol. Chem. 265, 13669-13676, 1990
 A>Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-ter
 A:Reference number: A37117; MUID:90337977; PMID:2143188
 A:Contents: annotation; hementin cleavage site
 A>Note: hementin, a protease from Haemaphysalis gilliamii, the giant South American leech,
 R:Stencker, L.; Sillard, R.; Bensch, K.W.; Rut, A.; Kaida, M.; Schulz-Knappe, P.; Schep
 Biochem. Biophys. Res. Commun. 215, 896-902, 1995
 A>Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites and
 A:Reference number: J4334; MUID:96027996; PMID:7488058
 A:Contents: annotation; composition and amino-terminal sequences of carboxyl end peptide
 C:Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
 C:Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
 C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves
 ization sites responsible for the formation of the soft clot.
 C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
 ger) and between alpha chains (weaker) of different monomers.
 C:Comment: All fibrinogen chains are synthesized in the liver.
 C:Comment: See PIR:D44234 for the minor alternative splice form.
 C:Genetics:
 A:Gene: GDB:FCG
 A:Cross-references: GDB:119129; OMIM:134820
 A:Map position: 4q28-4q28
 A:Introns: 18/3; 60/3; 122/1; 171/2
 A>Note: The list of introns is incomplete
 C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see i
 ns are contained in the core. Two three-chain coiled coils emerge from this core and cor
 from the distal domain nodes.
 C:Function:
 A>Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into f
 A:Pathway: blood coagulation
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C:Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein; liver; p
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-629/Product: fibrinogen alpha chain #status experimental <MAT>
 F:20-35/Product: fibrinopeptide A #status experimental <APT>
 F:36-629/Product: fibrin alpha chain #status experimental <FCA>
 F:36-38/Region: polymerization site, binding to the distal domain of the gamma chain of
 F:57-185/Domain: fibrinogen disulfide ring homology <FDR>
 F:591-593/Region: cell attachment (R-G-D) motif
 F:22-46/Binding site: phosphate (Ser) (covalent) #status experimental
 F:33-36/Cleavage site: Arg-61y (thrombin) #status experimental
 F:47/Disulfide bonds: interchain (to alpha-47) #status experimental
 F:55/Disulfide bonds: interchain (to beta-95) #status experimental
 F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
 F:68/Disulfide bonds: interchain (to beta-106) #status experimental
 F:180/Disulfide bonds: interchain (to gamma-165) #status experimental
 F:184/Disulfide bonds: interchain (to beta-223) #status experimental
 F:288,419/Binding site: carboxylate (Asn) (covalent) #status absent
 F:322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
 F:347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status expe
 F:461-491/Disulfide bonds: #status experimental
 F:527,558,575,581,595/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status i

Query Match	100.0%	Score 83	DB 1	Length 644
Best Local Similarity	100.0%	Pred. No. 3.4e-05		
Matches	16	Conservative 0	Mismatches 0	Indels 0
Gaps	0			

1 ADSEGDPLAEGGCV 16

20 ADSEGDPLAEGGCV 35

RESULT 2

D44234
 fibrinogen alpha chain precursor, extended splice form - human
 N/Alternate names: coagulation factor I


```

A:Contains: fibrinopeptide A
C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: D44234; B44234
R:F.U. Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redman
Biochemistry 31, 11968-11972, 1992
A:Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel
A:Reference number: A44234; MUID:93090725; PMID:1457396
A:Accession: D44234
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA; DNA
A:Residues: 1-866 <FU>
A:Cross-references: UNIPROT:P02671; GB:M56569; NID:G182406; PID:G182407
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
A:Accession: B44234
A:Molecule type: mRNA; DNA
A:Residues: 605-866 <FU2>
A:Note: sequence extracted from NCBI backbone (NCBIF:119917)
C:Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
C:Genetics:
A:Gene: GDB:FGA
A:Cross-references: GDB:119129; OMIM:134820
A:Map position: 4q28-4q28
A:Introns: 18/3; 60/3; 122/1; 171/2
A:Note: the list of introns is incomplete
C:Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentical
nated in the core. Two three-chain coiled coils emerge from this core and connect it to
distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A:Pathway: blood coagulation
C:Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
C:Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F:20-35/Product: fibrinopeptide A #status experimental <APR>
F:36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F:57-186/Domain: fibrinogen disulfide ring homology <FDR>
F:591-593/Region: cell attachment (R-G-D) motif
F:629-863/Domain: fibrinogen beta/gamma homology <FBG>
F:22-460/Binding site: phosphate (Ser) (covalent) #status experimental
F:35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F:47/Disulfide bonds: interchain (to alpha-47) #status experimental
F:55/Disulfide bonds: interchain (to beta-95) #status experimental
F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
F:68/Disulfide bonds: interchain (to beta-106) #status experimental
F:180/Disulfide bonds: interchain (to gamma-165) #status experimental
F:184/Disulfide bonds: interchain (to beta-223) #status experimental
F:288,419/Binding site: carboxylate (Asn) (covalent) #status absent
F:322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F:347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F:461-491/Disulfide bonds: #status experimental
F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
F:686,831/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 83; DB 2; Length 866;
Best Local Similarity 100.0%; Pred. No. 4-66-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSEGDPLAEGGVR 16
Db 20 ADSEGDPLAEGGVR 35

RESULT 3
129501
fibrinopeptide A - baboon

```

```
C.Species: Papio sp., (baboon)
C.Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
C.Accession: A29501
R.Blomback, B.; Blomback, M.; Hann, C.
unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Ser
A.Reference number: A29501
A.Accession: A29501
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-16 <BIO>
C.Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match          96.4%; Score 80; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDPLAEGGGVR 16
       ||:|||||
Db      1 ADTGEDPFLAEGGGVR 16

RESULT 4
B24180
fibrinogen alpha chain - red guenon (fragment)
N.Contains: fibrinopeptide A
C.Species: Erythrocebus patas (red guenon, husar)
C.Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C.Accession: B24180
R.Nakamura, S.; Takenaka, O.; Takahashi, K.
J.Biochem. 97, 1487-1492, 1985
A.Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E
uenons, and baboons.
A.Reference number: A91990; MID:85289140; PMID:3928610
A.Accession: B24180
A.Molecule type: protein
A.Residues: 1-16 <NAK>
C.Cross-references: UNIPROT:P12803
C.Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match          96.4%; Score 80; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDPLAEGGGVR 16
       ||:|||||
Db      1 ADTGEDPFLAEGGGVR 16

RESULT 5
A24180
fibrinogen alpha chain - Japanese macaque (fragment)
N.Contains: fibrinopeptide A
C.Species: Macaca fuscata (Japanese macaque)
C.Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C.Accession: A24180
R.Nakamura, S.; Takenaka, O.; Takahashi, K.
J.Biochem. 97, 1487-1492, 1985
A.Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E
uenons, and baboons.
A.Reference number: A91990; MID:85289140; PMID:3928610
A.Accession: A24180
A.Molecule type: protein
A.Residues: 1-16 <NAK>
C.Cross-references: UNIPROT:P12803
C.Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match          96.4%; Score 80; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDPLAEGGGVR 16
       ||:|||||
Db      1 ADTGEDPFLAEGGGVR 16
```

RESULT 6

B28854

Fibrinopeptide A - hamadryas baboon

C/Species: Papio hamadryas (hamadryas baboon)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004

C/Accession: B28854

R/Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 94, 1973-1978, 1983

A/Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus)

A/Reference number: A91973; MUID:84161822; PMID:6423621

A/Accession: B28854

A/Molecule type: protein

A/Residues: 1-16 <NAK>

A/Cross-references: UNIPROT:P12803

C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 96.4%; Score 80; DB 2; Length 16;

Best Local Similarity 93.8%; Pred. No. 2.2e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADTGGDFLAEGGVR 16

DB 1 ADTGGDFLAEGGVR 16

RESULT 7

C28854

Fibrinopeptide A - gelada baboon

C/Species: Theropithecus gelada (gelada baboon)

C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004

C/Accession: C28854

R/Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 94, 1973-1978, 1983

A/Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus)

A/Reference number: A91973; MUID:84161822; PMID:6423621

A/Accession: C28854

A/Molecule type: protein

A/Residues: 1-16 <NAK>

A/Cross-references: UNIPROT:P12803

C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 96.4%; Score 80; DB 2; Length 16;

Best Local Similarity 93.8%; Pred. No. 2.2e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADTGGDFLAEGGVR 16

DB 1 ADTGGDFLAEGGVR 16

RESULT 8

A28854

Fibrinopeptide A - olive baboon

C/Species: Papio anubis, Papio hamadryas anubis (olive baboon)

C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004

C/Accession: A28854

R/Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 94, 1973-1978, 1983

A/Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus)

A/Reference number: A91973; MUID:84161822; PMID:6423621

A/Accession: A28854

A/Molecule type: protein

A/Residues: 1-16 <NAK>

A/Cross-references: UNIPROT:P12803

C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 96.4%; Score 80; DB 2; Length 16;

Best Local Similarity 93.8%; Pred. No. 2.2e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADTGGDFLAEGGVR 16

Db 1 ADTGGDFLAEGGVR 16

RESULT 9

H29501

Fibrinopeptide A - gray seal

C/Species: Halichoerus grypus (gray seal)

C/Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004

C/Accession: H29501

R/Blomback, B.; Blomback, M.; Hann, C.

unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Serology of the Order Carnivora

A/Reference number: A29501

A/Accession: H29501

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 <BLO>

A/Cross-references: UNIPROT:Q7M316

C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide ring homology

Query Match 74.7%; Score 62; DB 2; Length 16;

Best Local Similarity 80.0%; Pred. No. 0.0015;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DSGEGDFLAEGGVR 16

DB 2 DTKESDFLAEGGVR 16

RESULT 10

G29501

Fibrinopeptide A - bear

C/Species: Ursus sp. (bear)

C/Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004

C/Accession: G29501

R/Blomback, B.; Blomback, M.; Hann, C. unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Serology of the Order Carnivora

A/Reference number: A29501

A/Accession: G29501

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 <BLO>

A/Cross-references: UNIPROT:Q7M317

C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide ring homology

Query Match 73.5%; Score 61; DB 2; Length 16;

Best Local Similarity 73.3%; Pred. No. 0.0021;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DSGEGDFLAEGGVR 16

DB 2 DKEGEFLEAGGVR 16

RESULT 11

A05296

Fibrinogen alpha chain - dog (fragment)

C/Species: Canis lupus familiaris (dog)

C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004

C/Accession: A94308; A03118; A37511; A05296; B37511; C03118

R/Birken, S.; Wilner, G.D.; Canfield, R.E.

Thromb. Res. 7, 599-610, 1975

A/Title: Studies of the structure of canine fibrinogen.

A/Reference number: A94308; MUID:76081726; PMID:1198547

A/Accession: A94308

A/Molecule type: protein

A/Residues: 1-28 <BIR>

A/Cross-references: UNIPROT:P02673

R/Blomback, B.; Blomback, M.; Grendahl, N.J.

Acta Chem. Scand. 19, 1789-1791, 1965

A/Title: Studies on fibrinopeptides from mammals.

A/Reference number: A03118

A/Accession: A03118

A:Molecule type: protein
 A:Residues: 1-16 <BLO>
 R:Obstet. J., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.
 Biochem. Biophys. Res. Commun. 14, 555-558, 1964
 A:Reference number: A37511; MUID:66020594; PMID:5836555
 A:Accession: A37511
 A:Molecule type: protein
 A:Residues: 1, 'D', '3', 'EGKO', 8-16 <OSB>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C:Keywords: blood coagulation; liver; phosphoprotein; plasma
 F:1-16/Product: fibrinopeptide A #status experimental <APr>
 F:3/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 72.3%; Score 60; DB 2; Length 28;
 Best Local Similarity 73.3%; Pred. No. 0.0055;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 DSGEGDPLAEGGVR 16
 : |||: |||||
 Db 2 NSKEGFLEAGGVR 16

RESULT 12
 B29501
 fibrinopeptide A - European moose
 C:Species: Alces alces alces (European moose, elk)
 C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004
 C:Accession: B29501
 R:Blomback, B.; Blomback, M.; Hann, C.
 unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Sex
 A:Reference number: A29501
 A:Accession: B29501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <BLO>
 A:Cross-references: UNIPROT:Q7M315
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 69.9%; Score 58; DB 2; Length 19;
 Best Local Similarity 68.8%; Pred. No. 0.0076;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ADSGEDPLAEGGVR 16
 : |||: |||||
 Db 4 SDPAGSFLEAGGVR 19

RESULT 13
 A05294
 fibrinogen alpha chain - bovine (fragments)
 N:Contains: fibrinopeptide A
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 05-Jun-1987 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
 C:Accession: A05294; A25715; A03117; A37505; A37506; A37507; B37505; C03117
 R:Henschen, A.; Lottepeich, F.; Topfer-Petersen, E.; Kehl, M.; Timpl, R.
 in: Proceedings of the Biological Fluids, Proc. 28th Colloq., ed. Peeters, H., pp. 47-50, Per
 A:Reference number: A05294
 A:Accession: A05294
 A:Molecule type: protein
 A:Residues: 20-26, 'Y', 28-49; 55-80; 81-108 <HEN>
 A:Cross-references: UNIPROT:P02672
 R:Chung, D.W.; Rixon, M.W.; Davie, E.W.
 in: Proteins in Biology and Medicine, Bradshaw, R.A., ed., pp. 309-328, Academic Press, Ne
 A:Title: The biosynthesis of fibrinogen and the cloning of its cDNA.
 A:Reference number: A25715
 A:Accession: A25715
 A:Molecule type: mRNA
 A:Residues: 109-311 <CHU>
 R:Sjogquist, J.; Blomback, B.; Wallen, P.
 Ark. Kent 16, 425-436, 1960
 A:Title: Amino acid sequence of bovine fibrinopeptides.
 A:Reference number: A03117
 A:Accession: A03117

A:Molecule type: protein
 A:Residues: 1-19 <SJO>
 R:Folk, J.E.; Gladner, J.A.; Levin, Y.
 J. Biol. Chem. 234, 2317-2320, 1959
 A:Title: Thrombin-induced formation of co-fibrin. III. Acid degradation studies and sum
 A:Reference number: A37505
 A:Accession: A37505
 A:Molecule type: protein
 A:Residues: 1-19 <FOL>
 R:Timpl, R.; Pietrek, P.P.; Machter, E.; van Delden, V.
 Biochim. Biophys. Acta 490, 420-429, 1977
 A:Title: Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. II. Isolation
 A:Reference number: A37506; MUID:77112616; PMID:836881
 A:Accession: A37506
 A:Molecule type: protein
 A:Residues: 20-54 <TIM>
 R:Martinelli, R.A.; Ingilis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
 A:Reference number: A37507; MUID:79164394; PMID:434821
 A:Accession: A37507
 A:Molecule type: protein
 A:Residues: 23-52 <MAR>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C:Keywords: blood coagulation; liver; plasma
 F:1-19/Product: fibrinopeptide A #status experimental <APr>
 F:20-31/Product: fibrinogen alpha chain (fragments) #status experimental <MAT>

Query Match 69.9%; Score 58; DB 2; Length 311;
 Best Local Similarity 68.8%; Pred. No. 0.14;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 ADSGEDPLAEGGVR 16
 : |||: |||||
 Db 4 SDPSPGFLTEGGVR 19

RESULT 14
 F29501
 fibrinopeptide A - wombat
 C:Species: Vombatidae gen. sp. (wombat)
 C:Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
 C:Accession: F29501
 R:Blomback, B.; Blomback, M.; Hann, C.
 unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Sex
 A:Reference number: A29501
 A:Accession: F29501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <BLO>
 A:Cross-references: UNIPROT:Q7M318
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 68.7%; Score 57; DB 2; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.0085;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 EGDPLAEGGVR 16
 : |||: |||||
 Db 4 EGSFLAEGGVR 15

RESULT 15
 E29501
 fibrinopeptide A - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004
 C:Accession: E29501
 R:Blomback, B.; Blomback, M.; Hann, C.
 unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Sex
 A:Reference number: A29501
 A:Accession: E29501
 A:Molecule type: protein

A;Residues: 1-17 <BLO>
 A;Cross-references: UNIPROT:P14460
 R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
 Acta Chem. Scand. 19, 1789-1791, 1965
 A;Title: Studies on fibrinopeptides from mammals.
 A;Reference number: A03118
 A;Contents: annotation; confirmation of species assignment
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 66.3%; Score 55; DB 2; Length 17;
 Best Local Similarity 83.3%; Pred. No. 0.02;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGDFLAEGGGYR 16
 :|:|||||||
 Db 6 KGEFLAEGGGYR 17

Search completed: January 21, 2005, 08:31:39
 Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 91 Seconds

(without alignments)
101.165 Million cell updates/sec

Title: US-09-845-765-1
Perfect score: 83
Sequence: 1 ADSEGDPLAEGGVR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	218	2	Q8MW76 O8MW76 homo sapien
2	83	100.0	289	2	Q6NSD8 O6NSD8 homo sapien
3	83	100.0	289	2	A8H70246 A8H70246 homo sapi
4	83	100.0	866	1	F1BA_HUMAN F02671 homo sapien
5	80	96.4	16	1	F1BA_MACPU P12803 macaca fusc
6	76	91.6	16	1	F1BA_HYLLA P1453 hylobates 1
7	71	85.5	16	1	F1BA_MANLE P1455 mandrillus
8	65	78.3	18	1	F1BA_CAMDR P1444 camelus dro
9	64	77.1	19	1	F1BA_BISBO P1441 bison bonas
10	62	74.7	15	1	F1BA_SYNCA P1463 cyncerus ca
11	62	74.7	16	1	F1BA_CERSI P14535 ceratotheri
12	62	74.7	16	2	Q7M316 Q7M317 ursus sp. (
13	61	73.5	18	1	F1BA_LAMGL P1454 lama glama
14	61	73.5	18	1	F1BA_CANFA P02673 canis famli
15	60	72.3	28	1	F1BA_FELCA P1450 felis silve
16	59	71.1	16	1	F1BA_TAPPE P14536 capitus ter
17	59	71.1	16	1	F1BA_BUBBU P1442 bubalus bub
18	59	71.1	19	1	F1BA_ODOHE P1459 odocolleus
19	58	69.9	19	1	F1BA_CERLU P1446 cervus elap
20	58	69.9	19	1	Q7M315 Q7M315 alces alces
21	58	69.9	19	2	P02672 P02672 bos taurus
22	58	69.9	19	2	Q7M318 Q7M318 vombatidae
23	57	68.7	15	2	P1457 P1457 muntiacus m
24	56	67.5	19	1	F1BA_PIG P1451 ovis aries
25	55	66.3	19	1	Q7M319 Q7M319 macropus sp
26	55	66.3	19	1	F1BA_EQUUS P1449 equus asinu
27	54	65.1	16	1	F1BA_CERNI P1447 cervus nipp
28	54	65.1	19	1	F1BA_HORSE P1452 equus cabal
29	53	63.9	14	1	Q99K47 Q99K47 mus musculu
30	53	63.9	14	1	
31	52	62.7	557	2	

32	49	59.0	501	2	Q6U61 Q6U61 oryza sativ
33	49	59.0	501	2	A8Q56514 A8Q56514 oryza sat
34	47	56.6	19	1	F1BA_RANTA P1462 rangifer ta
35	47	56.6	200	2	Q9XFA0 Q9XFA0 ipomoea bat
36	46	55.4	223	2	Q84SN5 Q84SN5 aster tripo
37	46	55.4	223	2	Q9C679 Q9C679 arabidopsis
38	46	55.4	286	2	Q6M0G6 Q6M0G6 methanococ
39	46	55.4	286	2	CAP29861 CAP29861 methanoc
40	46	55.4	288	2	Q8U257 Q8U257 pyrococcus
41	45	54.2	79	2	Q8RUJ7 Q8RUJ7 helianthus
42	45	54.2	161	2	Q9AS45 Q9AS45 oryza sativ
43	45	54.2	226	2	Q6ILJ2 Q6ILJ2 drosophila
44	45	54.2	435	2	Q6FT0 Q6FT0 erwinia amy
45	45	54.2	435	2	Q8GFN7 Q8GFN7 citrobacter

ALIGNMENTS

RESULT 1

ID	Q8MW76	PRELIMINARY:	PRT:	218 AA.
AC	Q8MW76:			
DT	01-MAR-2002 (TREMBlrel. 20, Created)			
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)			
DE	01-MAR-2002 (TREMBlrel. 20, Last annotation update)			
DE	FGA protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
EX	MEDLINE=22386257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mulahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,			
RA	Krzywnicki M.I., Skalek U., Smaluk D.E., Scherch A., Schein J.E.,			
RA	Jones S.J., Maitra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Strausberg R.,			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC020764; A8H20764.1; -.			
DR	HSSP; P02671; IFZA.			
SQ	SEQUENCE 218 AA; 24695 MW; 36D756A8116EA94A CRC64;			

Query Match 100.0%; Score 83; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ADSEGDPLAEGGVR 16
Db	20	ADSEGDPLAEGGVR 35

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RESULT 2
Q6NSD8      PRELIMINARY;      PRT;      289 AA.
ID Q6NSD8;
AC Q6NSD8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FGA protein.
GN Name=FGA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carinci P., Prange C.,
RA Rana S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070246; AAH70246.1; -.
SQ SEQUENCE 289 AA; 3291 MW; 1CFAECBA37F73BA0 CRC64;

Query Match      100.0%; Score 83; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSEGDPLAEGGVR 16
      |||||
      20 ADSEGDPLAEGGVR 35

RESULT 3
AAH70246      PRELIMINARY;      PRT;      289 AA.
ID AAH70246;
AC AAH70246;
DT 24-MAY-2004 (TREMBlrel. 27, Created)
DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT 24-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE FGA protein.
GN FGA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carinci P., Prange C.,
RA Rana S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070246; AAH70246.1; -.
SQ SEQUENCE 289 AA; 3291 MW; 1CFAECBA37F73BA0 CRC64;

Query Match      100.0%; Score 83; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSEGDPLAEGGVR 16
      |||||
      20 ADSEGDPLAEGGVR 35

RESULT 4
FIBA_HUMAN      STANDARD;      PRT;      866 AA.
ID FIBA_HUMAN;
AC P02671; Q9BX62; Q9UCH2;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen alpha/alpha-E chain precursor [contains: fibrinopeptide A].
GN Name=FGA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RX MEDLINE=93090725; PubMed=1457396;
RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA Roy S.N., Redman C.M., Grieninger G.;
RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT subunit: a novel exon conferring marked homology to beta and gamma
RT subunits."
RL Biochemistry 31:11968-11972(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RA Chung D.W., Grieninger G.;
RT "Fibrinogen DNA and protein sequences."
RL (in) Ebert R.F. (eds.).
RL Index of variant human fibrinogens, pp.13-24, CRC Press, Boca Raton
RL (1994).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
RP ALA-456.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNPS, NHLBI HUG6682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carinci P., Prange C.,
RA Rana S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070246; AAH70246.1; -.
SQ SEQUENCE 289 AA; 3291 MW; 1CFAECBA37F73BA0 CRC64;

Query Match      100.0%; Score 83; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSEGDPLAEGGVR 16
      |||||
      20 ADSEGDPLAEGGVR 35

RESULT 4
FIBA_HUMAN      STANDARD;      PRT;      866 AA.
ID FIBA_HUMAN;
AC P02671; Q9BX62; Q9UCH2;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen alpha/alpha-E chain precursor [contains: fibrinopeptide A].
GN Name=FGA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RX MEDLINE=93090725; PubMed=1457396;
RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA Roy S.N., Redman C.M., Grieninger G.;
RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT subunit: a novel exon conferring marked homology to beta and gamma
RT subunits."
RL Biochemistry 31:11968-11972(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RA Chung D.W., Grieninger G.;
RT "Fibrinogen DNA and protein sequences."
RL (in) Ebert R.F. (eds.).
RL Index of variant human fibrinogens, pp.13-24, CRC Press, Boca Raton
RL (1994).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
RP ALA-456.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNPS, NHLBI HUG6682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
[4]

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RP SEQUENCE OF 1-655 FROM N.A. (ISOFORM ALPHA-E).
 RC TISSUE=Liver;
 RX MEDLINE=91344740; PubMed=2102623;
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 fibrinogen.";
 RL Adv. Exp. Med. Biol. 281:39-48(1990).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=83247396; PubMed=6575389;
 RA Kant J.A., Lord S.T., Crabtree G.R.;
 RT "Partial mRNA sequences for human A alpha, B beta, and gamma
 fibrinogen chains: evolutionary and functional implications";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
 RN [6]
 RP SEQUENCE OF 1-629 FROM N.A.
 RX MEDLINE=83283432; PubMed=6688355;
 RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 the alpha chain of human fibrinogen.";
 RL Biochemistry 22:3237-3244(1983).
 RN [7]
 RP SEQUENCE OF 20-629.
 RA Henschen A., Lotzpeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 structural variants.";
 RL (in) Peeters H. (eds.);
 RL Proceedings of the biological fluids, Proc. 28th colloquium, pp.51-56,
 Pergamon Press, Oxford (1980).
 RN [8]
 RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
 RX MEDLINE=80088231; PubMed=518846;
 RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
 Overlapping sequences providing the complete sequence.";
 RL Biochemistry 18:5410-5416(1979).
 RN [9]
 RP SEQUENCE OF 110-156 FROM N.A.
 RX MEDLINE=84069777; PubMed=6689067;
 RA Tramm A.M., Bacon M.A., Williamson R., Humphries S.;
 RT "Isolation and characterization of cDNA clones for the A alpha- and
 gamma-chains of human fibrinogen.";
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [10]
 RP SEQUENCE OF 605-644 FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=83253384; PubMed=6575700;
 RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
 RT "Cloning of fibrinogen genes and their cDNA.";
 RL Ann. N. Y. Acad. Sci. 408:449-456(1983).
 RN [11]
 RP SEQUENCE OF 20-35.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 RN [12]
 RP CROSS-LINKING ACCEPTOR SITES.
 RX MEDLINE=80088230; PubMed=518845;
 RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
 Exact location of cross-linking acceptor sites.";
 RL Biochemistry 18:5405-5410(1979).
 RN [13]
 RP CROSS-LINKING ACCEPTOR SITES.
 RX MEDLINE=78130085; PubMed=632262;
 RA Fretio L.J., Ferguson E.W., Steilman H.M., McKee P.A.;
 RT "Localization of the alpha-chain cross-link acceptor sites of human
 fibrin.";
 RL J. Biol. Chem. 253:2184-2195(1978).
 RN [14]
 RP VARIANT, AND DISULFIDE BONDS.
 RX MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hassel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RN [15]
 RP Thromb. Res. 8:639-658(1976).
 RN [15]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [16]
 RP CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
 RX MEDLINE=87057190; PubMed=2877981;
 RA Kimura S., Aoki N.;
 RT "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
 RL J. Biol. Chem. 261:15591-15595(1986).
 RN [17]
 RP PHOSPHORYLATION.
 RX MEDLINE=84104274; PubMed=6318767;
 RA Itarte E., Piana M., Guasch M.D., Marcos C.;
 RT "Phosphorylation of fibrinogen by casein kinase 1.";
 RL Biochem. Biophys. Res. Commun. 117:631-636(1983).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
 RX MEDLINE=92218459; PubMed=1560020;
 RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
 RT "The structure of residues 7-16 of the A alpha-chain of human
 fibrinogen bound to bovine thrombin at 2.3-A resolution.";
 RL J. Biol. Chem. 267:7911-7920(1992).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
 RX MEDLINE=97472408; PubMed=9332333;
 RA Spraggon G., Evere S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
 RX MEDLINE=98292395; PubMed=9628725;
 RA Evere S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
 RX MEDLINE=98356117; PubMed=9689040;
 RA Spraggon G., Applegate D., Evere S.J., Zhang J.Z., Veerapandian L.,
 RA Redman C., Doolittle R.F., Grieninger G.;
 RT "Crystal structure of a recombinant alphaBEC domain from human
 fibrinogen-420.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=99175089; PubMed=10074346;
 RA Evere S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 RN [23]
 RP VARIANT KYOTO-2.
 RX MEDLINE=91300046; PubMed=2070049;
 RA Yoshida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
 RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
 characterized by the replacement of A alpha proline-18 by leucine.";
 RL Blood 78:149-153(1991).
 RN [24]
 RP VARIANT LIMA.
 RX MEDLINE=92340680; PubMed=1634621;
 RA Mekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
 RA Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H.,
 RA Perez-Requeno J.L., Matsuda M.;
 RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A alpha-arginine-
 141 to serine substitution associated with extra N-glycosylation at A
 alpha-asparagine-139. Impaired fibrin gel formation but normal fibrin-
 facilitated plasminogen activation catalyzed by tissue-type
 plasminogen activator.";
 RT

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RL J. Clin. Invest. 90:67-76(1992).
RN [25]
RP VARIANT CARACAS-2.
RX MEDLINE=91268018; PubMed=1675636;
RA Meekava H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
RA Arocha-Pinango C.L., Matsuda M.,
RT "An A alpha Ser-434 to N-glycosylated Aa substitution in a
RT dyafibrinogen, fibrinogen Caracas II, characterized by impaired fibrin
RT gel formation."
RL J. Biol. Chem. 266:11575-11581(1991).
RN [26]
RP VARIANT DUSART.
RX MEDLINE=93232289; PubMed=8473507;
RA Koopman J., Haverkate F., Grimbergen J., Lord S.T., Moseeson M.W.,
RA Dlorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
RA Caen J.P.;
RT "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and its
Query Match 100.0%; Score 83; DB 1; Length 866;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADGSGDFLAEGGVR 16
Db 20 ADGSGDFLAEGGVR 35

RESULT 5
FIBA_MACFU STANDARD; PRT; 16 AA.
ID FIBA_MACFU
AC P12803;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Macaca fuscata fuscata (Japanese macaque),
OS Macaca fascicularis (Crah eating macaque) (Cynomolgus monkey),
OS Macaca mulatta (Rhesus macaque),
OS Cercopithecus aethiops (Green monkey) (Griivet),
OS Erythrocebus patas (Red guenon) (Cercopithecus patas),
OS Papio anubis (Olive baboon),
OS Papio hamadryas (Hamadryas baboon), and
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
NCBI_TaxID=9543, 9541, 9544, 9534, 9538, 9555, 9557, 9565;
RN [1]
RP SEQUENCE.
RC SPECIES=E. patas, and M. fuscata;
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas
RT monkey (Erythrocebus patas): their amino acid sequences, restricted
RT mutations, and a molecular phylogeny for macaques, guenons, and
RT baboons."
RL J. Biochem. 97:1487-1492(1985).
RN [2]
RP SEQUENCE.
RC SPECIES=P. anubis, P. hamadryas, and T. gelada;
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and evolutionary
RT rates and a molecular phylogeny for the baboons."
RL J. Biochem. 94:1973-1978(1983).
RN [3]
RP SEQUENCE.
RC SPECIES=C. aethiops, M. mulatta, and M. fascicularis;
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates."

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RL Acta Chem. Scand. 19:1788-1789(1965).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR: A24180; A24180.
DR PIR: A28054; A28054.
DR PIR: B24180; B24180.
DR PIR: B28854; B28854.
DR PIR: C28854; C28854.
KW Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 16 Fibrinopeptide A.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1565 MW; 49898B63EA04D3 CRC64;

Query Match 96.4%; Score 80; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.5e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADGSGDFLAEGGVR 16
Db 1 ADTGEGBFLAEGGVR 16

RESULT 6
FIBA_HYLLA STANDARD; PRT; 16 AA.
ID FIBA_HYLLA
AC P14453;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Hylobates lar (Common gibbon).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBI_TaxID=9580;
RN [1]
RP SEQUENCE.
RX MEDLINE=70294424; PubMed=5466708;
RA Moses G.A., Doolittle R.F., Roberts B.F.;
RT "Gibbon fibrinopeptides: identification of a glycine-serine allelism
RT at position B-3."
RL Science 170:468-470(1970).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 16 Fibrinopeptide A.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1565 MW; 49898B63EA04D3 CRC64;

Query Match 91.6%; Score 76; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 0.00014;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADGSGDFLAEGGVR 16
Db 1 ADTGEGBFLAEGGVR 16

RESULT 7

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FIBRA_MANTLE
ID FIBRA_MANTLE STANDARD; PRT; 16 AA.
AC P1445;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FCA;
OS Mandrillius leucophaeus (Drill) (Papio leucophaeus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Mandrillius.
OX NCBI_TaxID=9568;
RN [1]
RP SEQUENCE.
RX MEDLINE=69115139; PubMed=4974768;
RA Doolittle R.F., Glasow C., Mrose G.A.;
RT "Characterization of fibrinopeptides A and B from a drill (Mandrillius
leucophaeus).";
RL Biochim. Biophys. Acta 175:217-219(1969).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
(alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
which cleaves fibrinopeptides A and B from alpha and beta chains,
and thus exposes the N-terminal polymerization sites responsible
for the formation of the soft clot.
KM Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 16
FT NON TER 1 16 Fibrinopeptide A.
SQ SEQUENCE 16 AA; 1567 MW; 08B8CB87BA051A4 CRC64;

Query Match 85.5%; Score 71; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.00082;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADGSGDFLAEGGVR 16
DB 1 ADTGDDGFTEGGVR 16

RESULT 8
FIBRA_CAMDR STANDARD; PRT; 18 AA.
ID FIBRA_CAMDR
AC P1444;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FCA;
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE.
RX MEDLINE=67209145; PubMed=6033721;
RA Doolittle R.F., Schubert D., Schwartz S.A.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
Dromedary camel, mule deer, and cape buffalo."
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FCA;
OS Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
(alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
which cleaves fibrinopeptides A and B from alpha and beta chains,
and thus exposes the N-terminal polymerization sites responsible
for the formation of the soft clot.
KM Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 18
FT NON TER 1 18
SQ SEQUENCE 18 AA; 1567 MW; 08B8CB87BA051A4 CRC64;

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FT PEPTIDE 1 18 Fibrinopeptide A.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1835 MW; 24448763D7F4CC6 CRC64;

Query Match 78.3%; Score 65; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.0076;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSGGDFLAEGGVR 16
DB 4 DADGDFLAEGGVR 18

RESULT 9
FIBRA_BISBO STANDARD; PRT; 19 AA.
ID FIBRA_BISBO
AC P1441;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FCA;
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
OC Bovinae; Bison.
OX NCBI_TaxID=9902;
RN [1]
RP SEQUENCE.
RX Blomback B., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RA Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
(alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
which cleaves fibrinopeptides A and B from alpha and beta chains,
and thus exposes the N-terminal polymerization sites responsible
for the formation of the soft clot.
KM Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 19
FT NON TER 1 19 Fibrinopeptide A.
SQ SEQUENCE 19 AA; 1836 MW; 9BA55A0F473B59C5 CRC64;

Query Match 77.1%; Score 64; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ADGSGDFLAEGGVR 16
DB 4 SDPASGDFLAEGGVR 19

RESULT 10
FIBRA_SYNCA STANDARD; PRT; 15 AA.
ID FIBRA_SYNCA
AC P1443;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FCA;
OS Syncerus caffer (Cape buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
OC Bovinae; Syncerus.
OX NCBI_TaxID=9970;
RN [1]
RP SEQUENCE.
RX MEDLINE=67209145; PubMed=6033721;
RA Doolittle R.F., Schubert D., Schwartz S.A.;

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RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT Diomedea camel, mule deer, and cape buffalo."
RL Arch. Biochem. Biophys. 118:456-467(1967).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KM Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 15 Fibrinopeptide A.
FT NON TER 1 15
SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5F0B41CC6 CRC64;

Query Match 74.7%; Score 62; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.018;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DSGEGDFLAEGGVR 16
DB 1 EDGSGEFLAEGGVR 15

RESULT 11
FIBA_CERSI STANDARD; PRT; 16 AA.
ID FIBA_CERSI
AC P14535;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_TaxID=9807;
RN [1]
RP SEQUENCE.
RA O'Neill P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KM Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 16 Fibrinopeptide A.
FT NON TER 1 16
SQ SEQUENCE 16 AA; 1639 MW; 0958CBB6293F4C81 CRC64;

Query Match 74.7%; Score 62; DB 1; Length 16;
Best Local Similarity 73.3%; Pred. No. 0.019;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 DSGEGDFLAEGGVR 16
DB 2 ETGEGDFLAEGGVR 16

RESULT 12
O7M316 PRELIMINARY; PRT; 16 AA.
ID O7M316
AC O7M316;
DT 01-MAR-2004 (TRENBLREL. 26, Created)
DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)

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DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Fibrinopeptide A.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Hann C.;
RL Unpublished results, cited by:
RL Blomback B., Blomback M.,
RL (In) Hawkes J.G. (eds.);
RL Chemoecology and Serology, pp.0:3-20, Academic Press, New York
RL (1968).
DR PIR: H29501; H29501.
SQ SEQUENCE 16 AA; 1682 MW; 4858DAF2319C4DC3 CRC64;

Query Match 74.7%; Score 62; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 DSGEGDFLAEGGVR 16
DB 2 DTKESDFLAEGGVR 16

RESULT 13
O7M317 PRELIMINARY; PRT; 16 AA.
ID O7M317
AC O7M317;
DT 01-MAR-2004 (TRENBLREL. 26, Created)
DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Fibrinopeptide A.
OS Ursus sp. (bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9641;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Hann C.;
RL Unpublished results, cited by:
RL Blomback B., Blomback M.;
RL (In) Hawkes J.G. (eds.);
RL Chemoecology and Serology, pp.0:3-20, Academic Press, New York
RL (1968).
DR PIR: G29501; G29501.
SQ SEQUENCE 16 AA; 1622 MW; 09598BB6318BD2C4 CRC64;

Query Match 73.5%; Score 61; DB 2; Length 16;
Best Local Similarity 73.3%; Pred. No. 0.027;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DSGEGDFLAEGGVR 16
DB 2 DKEGGEFLAEGGVR 16

RESULT 14
FIBA_LAMGL STANDARD; PRT; 18 AA.
ID FIBA_LAMGL
AC P14454;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Lama glama (Llama), and
OS Lama vicugna (Vicugna) (Vicugna vicugna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844, 9843;
RN [1]

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RP SEQUENCE.
RC SPECIES=L.glama;
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=L.vicugna;
RA Mroos G.A., Doollittle R.F.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides.",
RL Arch. Biochem. Biophys. 122:674-684(1967).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 18 Fibrinopeptide A.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1834 MW; 2444487B8B7F4C6 CRC64;

Query Match 73.5%; Score 61; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 0.031;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DSGEGDPLAEGGVR 16
| : : : : :
Db 4 DADKGFLEGGVR 18

RESULT 15
FIBA CANFA STANDARD; PRT; 28 AA.
ID FIBA CANFA STANDARD; PRT; 28 AA.
AC P02673; P14464;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Canis familiaris (Dog), and
OS vulpes vulpes (Red fox).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615, 9627;
RN [1]
RP SEQUENCE.
RC SPECIES=C.familiaris;
RX MEDLINE=76081726; PubMed=1198547;
RA Birken S., Wilner G.D., Canfield R.B.;
RT "Studies of the structure of canine fibrinogen.";
RL Thromb. Res. 7:599-610(1975).
RN [2]
RP SEQUENCE OF 1-16.
RC SPECIES=C.familiaris, and V.vulpes;
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [3]
RP SEQUENCE OF 1-16.
RC SPECIES=C.familiaris;
RX MEDLINE=66020594; PubMed=5836555;
RA Osbahr A.J. Jr., Colman R.W., Laki K., Gladner J.A.;
RT "The nature of the peptides released from canine fibrinogen.";
RL Biochem. Biophys. Res. Commun. 14:555-558(1964).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.

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CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; A94308; A05296.
KW Blood coagulation; Direct protein sequencing; Phosphorylation; Plasma.
FT PEPTIDE 1 16 Fibrinopeptide A.
FT MOD_RES 3 3 Phosphoserine (partial).
FT CONFLICT 2 2 N -> D (in Ref. 2).
FT CONFLICT 4 7 KEKE -> EKKQ (in Ref. 2).
FT NON_TER 28
SQ SEQUENCE 28 AA; 2958 MW; 09DCD3F923BFEBD2 CRC64;

Query Match 72.3%; Score 60; DB 1; Length 28;
Best Local Similarity 73.3%; Pred. No. 0.068;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DSGEGDPLAEGGVR 16
| : : : : :
Db 2 NSKEGFLEGGVR 16

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 Job time : 95 secs

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